




# Gerald Amiel Ballena

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## Professional Summary

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Experienced bioinformatician with a strong background in computational biology, phylogenetics, and metagenomics. Skilled in developing and optimizing pipelines for large-scale sequence analysis. Passionate about applying robust, innovative methodologies to solve complex biological problems.

## Experience

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**2024 – Present**

*University of the Philippines, College of Public Health*

**Project Technical Specialist**

## Education

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**University of the Philippines Diliman: M.S. Microbiology**

*Graduated: 2022*

**Thesis:** *[Insert Thesis Title]*

**Specifics:** *[Insert notable coursework or achievements]*

**University of the Philippines Baguio: B.S. Biology**

*Graduated: 2018*

**Thesis:** *[Insert Thesis Title]*

**Specifics:** *[Insert notable coursework or achievements]*

## Skills

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### Programming.....

**Languages:** Python, R, Bash, Perl

**Installation Toolkits:** BiocManager, upcxx

### Bioinformatics Tools.....

**Metagenomics:** Kraken2, MetaPhlAn, HUMAnN

**Assembly & Binning:** MEGAHIT, METAWRAP, CheckM

**Genomics:** CLC Workbench, Roary, MinHash

**Quality Control:** FastQC, BUSCO, QUAST    **Trimming:** Trimmomatic, Sickle, Cutadapt

**Phylogenetics:** RaxML, FastTree, IQ-TREE, phyML, BEAST

**Gene Ontology:** KEGG, GOseq

**Annotation:** Prokka, ShortBRED, EggNOG-mapper

**Others:** DESeq2, BBMap Suite, anvio-8, SPAdes

**Data Analysis & Visualization**.....

**Machine Learning:** scikit-learn, caret (R)

**Visualization:** ggplot2, Plotly, Krona, Shiny, Seaborn, Tableau

**Technical Skills**.....

**Version Control:** Git, GitHub

**High-Performance Computing:** Slurm

**Workflow Automation:** Snakemake, Conda, YAML (config files)

**Virtualization:** Docker, WSL2

**Other Tools**.....

**Technical Writing:** Overleaf, TeXStudio

**Collaboration:** Thunderbird, Notion, MS Word (mailing lists)

**Documentation:** TeXStudio, Jupyter Notebooks

**Certifications**

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**Fundamentals Courses**.....

**AI Fundamentals:** ..... Nov 2024

**Data Literacy:** ..... Nov 2024

**Beginner-Level Courses**.....

**Introduction to Data Engineering:** ..... Nov 2024

**Intermediate-Level Courses**.....

**Intermediate R:** ..... Nov 2024

**Introduction to Bioconductor in R:** ..... Nov 2024

**RNA-Seq with Bioconductor in R:** ..... Nov 2024

**Differential Expression Analysis with limma in R:** ..... Nov 2024

**ChIP-Seq with Bioconductor in R:** ..... Nov 2024

**Analyzing Genomic Data in R:** ..... Nov 2024

**Advanced-Level Courses**.....

**Hyperparameter Tuning in R:** ..... Nov 2024

**Designing Machine Learning Workflows in Python:** ..... Nov 2024

**Projects**

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For more details, visit [GitHub Documentation.pdf](#).....

**The Repositories**.....

**Project4:** Scripts related to metagenomics.

**Main:** Scripts for general use case scenarios, such as fetching Bioconda packages.

**Side:** Curiosity/exploration-driven scripts.

**Health:** Scripts related to living (or trying to live) a healthy lifestyle.  
**Finance: WIP;** scripts intended for personal finance management.

## Languages

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|--|---|
| <b>English:</b> Fluent                   | <i>Professional proficiency.</i>                            |
| <b>Tagalog:</b> Native                   | <i>Conversational</i>                                       |
| <b>Ilocano:</b> Can understand           | <i>Wernicke's area skill issue.</i>                         |
| <b>Computer Languages (For Fun).....</b> |   |
| <b>Python:</b> Fluent                    | <i>Fluent enough for advanced bioinformatics.</i>           |
| <b>R:</b> Advanced                       | <i>Best data visualization tool out there (currently).</i>  |
| <b>Bash:</b> Intermediate                | <i>Go-to shell scripting language.</i>                      |
| <b>Perl:</b> Fair                        | <i>Would rather "speak" in Bash.</i>                        |
| <b>C++:</b> Basic                        | <i>As fluent as someone who hasn't used it in a decade.</i> |

## References

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**Available upon request & only if already shortlisted.**